



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy
Search <u>Protein</u> <input type="checkbox"/> for <input type="text"/>						
		Limits	Preview/Index	History	Clipboard	
Display	GenPept	<input type="button" value="▼"/>	Save	Text	Add to Clipboard	

□1: P02932. OUTER MEMBRANE
PO...[gi:130121]

[BLink](#), [Related Sequences](#), [PubMed](#),
[Taxonomy](#), [LinkOut](#)

LOCUS PHOE_ECOLI 351 aa **BCT**
DEFINITION OUTER MEMBRANE PORE PROTEIN E PRECURSOR.
ACCESSION P02932
PID gi:130121
VERSION P02932 GI:130121
DBSOURCE swissprot: locus PHOE_ECOLI, accession P02932;
 class: standard.
 created: Jul 21, 1986.
 sequence updated: Jul 21, 1986.
 annotation updated: Aug 20, 2001.
 xrefs: gi: gi: 42389, gi: gi: 42391, gi: gi: 236
1786436, gi: gi: 4902908, gi: gi: 4902976, gi: g
1552809, gi: gi: 42495, gi: gi: 42496, gi: gi: 7
443180
 xrefs (non-sequence databases): SWISS-2DPAGE P02
 B037.0, EcoGene EG10729, InterPro IPR001702, Pfa
 PR00182, PRINTS PR00183, PROSITE PS00576
KEYWORDS Outer membrane; Transmembrane; Porin; Signal; 3D
 Complete proteome.
SOURCE Escherichia coli.
ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision; Ent
 Escherichia.
REFERENCE 1 (residues 1 to 351)
AUTHORS Overbeeke,N., Bergmans,H., van Mansfeld,F. and L
TITLE Complete nucleotide sequence of phoE, the struct
 phosphate limitation inducible outer membrane po
 Escherichia coli K12
JOURNAL J. Mol. Biol. 163 (4), 513-532 (1983)
MEDLINE 83189086
REMARK SEQUENCE FROM N.A.
 STRAIN=K12
REFERENCE 2 (residues 1 to 351)
AUTHORS Blattner,F.R., Plunkett,G.I.I.I., Bloch,C.A., Pe

Burland, V., Riley, M., Collado-Vides, J., Glasner, Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, Rose, D.J., Mau, B. and Shao, Y.

TITLE The complete genome sequence of *Escherichia coli*
JOURNAL *Science* 277 (5331), 1453-1474 (1997)
MEDLINE 97426617
REMARK SEQUENCE FROM N.A.
STRAIN=K12 / MG1655
REFERENCE 3 (residues 1 to 351)
AUTHORS Takemoto, K., Mori, H., Murayama, N., Kataoka, K., Yamamoto, Y., Inokuchi, H., Miki, T., Hatada, E., Ichihara, S., Mizuno, T., Makino, K., Nakata, A., Yu and Mizobuchi, K.
TITLE Direct Submission
JOURNAL Submitted (??-FEB-1996)
REMARK SEQUENCE FROM N.A.
STRAIN=K12 / W3110
REFERENCE 4 (residues 1 to 351)
AUTHORS Schramm, S., Duncan, M., Allen, E., Araujo, R., Apar, Davis, K., Federspiel, N., Hyman, R., Kalman, S., Ko Lashkari, D., Lew, H., Lin, D., Namath, A., Oefner, P Davis, R.W.
TITLE Direct Submission
JOURNAL Submitted (??-SEP-1996)
REMARK SEQUENCE FROM N.A.
REFERENCE 5 (residues 1 to 351)
AUTHORS Deutch, A.H., Rushlow, K.E. and Smith, C.J.
TITLE Analysis of the *Escherichia coli* proBA locus by sequencing
JOURNAL *Nucleic Acids Res.* 12 (15), 6337-6355 (1984)
MEDLINE 84297232
REMARK SEQUENCE OF 1-22 FROM N.A.
REFERENCE 6 (residues 1 to 351)
AUTHORS Struyve, M., Moons, M. and Tommassen, J.
TITLE Carboxy-terminal phenylalanine is essential for assembly of a bacterial outer membrane protein
JOURNAL *J. Mol. Biol.* 218 (1), 141-148 (1991)
MEDLINE 91162638
REMARK MUTAGENESIS OF PHE-351.
REFERENCE 7 (residues 1 to 351)
AUTHORS Jap, B.K., Walian, P.J. and Gehring, K.
TITLE Structural architecture of an outer membrane chain by electron crystallography
JOURNAL *Nature* 350 (6314), 167-170 (1991)
MEDLINE 91172301
REMARK X-RAY CRYSTALLOGRAPHY (6.0 ANGSTROMS).

REFERENCE 8 (residues 1 to 351)
 AUTHORS Cowan, S.W., Schirmer, T., Rummel, G., Steiert, M.,
 Paupit, R.A., Jansonius, J.N. and Rosenbusch, J.P.
 TITLE Crystal structures explain functional properties
 porins
 JOURNAL Nature 358 (6389), 727-733 (1992)
 MEDLINE 92375189
 REMARK X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 REFERENCE 9 (residues 1 to 351)
 AUTHORS Struyve, M., Visser, J., Adriaanse, H., Benz, R. and
 TITLE Topology of PhoE porin: the 'eyelet' region
 JOURNAL Mol. Microbiol. 7 (1), 131-140 (1993)
 MEDLINE 93172954
 REMARK TOPOLOGY.
 COMMENT -----
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 collaboration between the Swiss Institute of Bio
 the EMBL outstation - the European Bioinformatic
 The original entry is available from <http://www.ebi.ac.uk/sprot>

 [FUNCTION] THIS IS ONE OF THE PROTEINS INDUCED WHEN
 ARE GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN
 PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC
 PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIV
 SOLUTES.
 [SUBUNIT] HOMOTRIMER.
 [SUBCELLULAR LOCATION] INTEGRAL MEMBRANE PROTEIN
 [SIMILARITY] BELONGS TO THE OMPC/PHOE FAMILY OF
 FEATURES Location/Qualifiers
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 Protein 1..351
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 Region 22..351
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 Region 25..26
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 Region 30..35
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 Region 37..45

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Region /region_name="Hydrogen bonded turn" 120..123
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181 vkkqngdgfg tslytdfggs dfaisgaytn sdrtneqnlp srgtgp
241 niylatfyse trkmtpitgg fanktqnfea vaqyqfdffg1 rpslgy
301 dlvnyidvqa tyyfnknmsa fvdykingld sdnklninnd divavq

11

Revised: October 24, 2001.

